

GAATTCGGGAACGGCCACAGCAGCTGCTGAGCC[ATGGCTGAAGGGGAAATCACACCTTCACAGCCCTGACCGAGAAGTTTAAAT
89
A E G E I T T F T A L T E K F N
16
CTGCCTCCAGGGAATTACAAGAAGCCCAACTCCTCTACTGTAGCAACGGGGGCCACTTCCTGAGGATCCTTCCGGATGGCACAGTGGAT
178
L P P G N Y K K P K L L Y C S N G G H F L R I L P D G T V D
46
GGGACAAAGGACAGGAGCGACGACACATTTCAGCTGCAGCTCAGTGCAGGAAAGCGTGGGGAGGTGTATATAAGAGTACCGAGACTGGC
277
G T R D R S D Q H I Q L Q L S A E S V G E V Y I K S T E T G
76
CAGTACTTGGCCATGGACACCGGCGCTTTTATACGGCTCACAGACACCAATGAGGAATGTTTCTCTGGAAAGGCTGGAGGAGAAC
356
Q Y L A M D T D G L L Y G S Q T P N E E C L F L E R L E N
106
CATTACAACACCTATATATCCAAGAAGCATGCAGAGAAGAATTGGTTTGGCTCAAGAAGAATGGGAGCTGCAAAACGGGTCCTCGG
445
H Y N T Y I S K K H A E K N W F V G L K K N G S C K R G P R
CAAACGGGTCCTAAA
K
136
ACTCACTATGGCCAGAAAGCAATCTTGTCTCTCCCTGCCAGTCTCTTCIGATT]AAAGAGATCTGTTCTGGTGTGACCACTCCAGAGA
534
T H Y G Q K A I L F L P L P V S S D
154
ACTCACTATGGCCAG
AGTTTCGAGGGTCCCTCACCTGGTTGACCCCAAAATGTTCCCTTGACCATTTGGCTGCGCTAACCCCGAGCCACAGAGCCTGAATTTGT
623
AAGCAACTT
632

FIGURE 1

10032554-121704

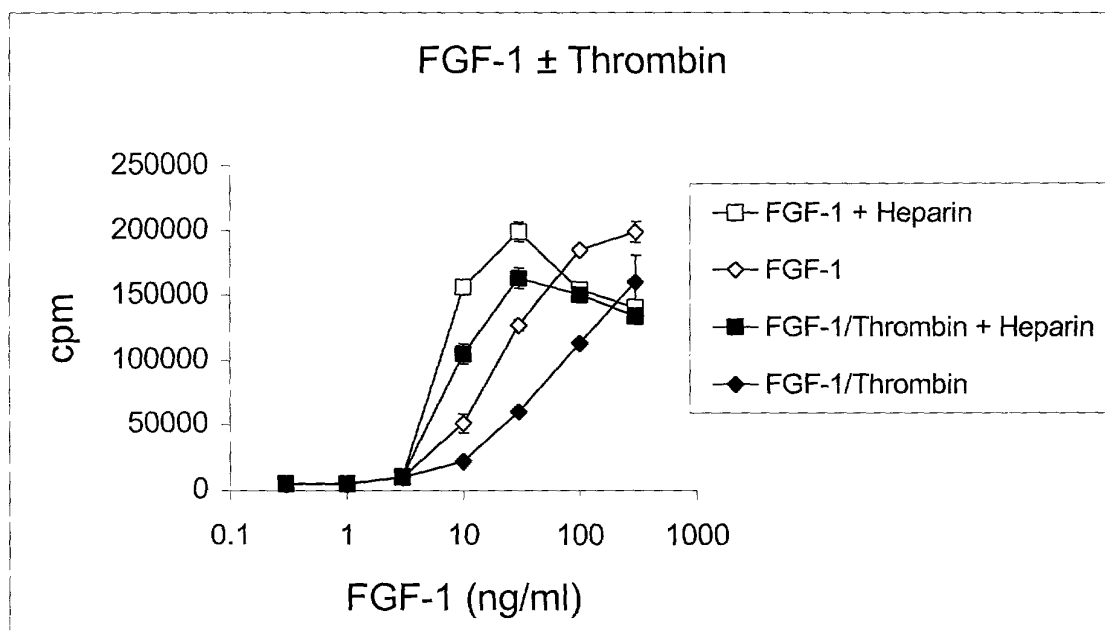


FIGURE 2

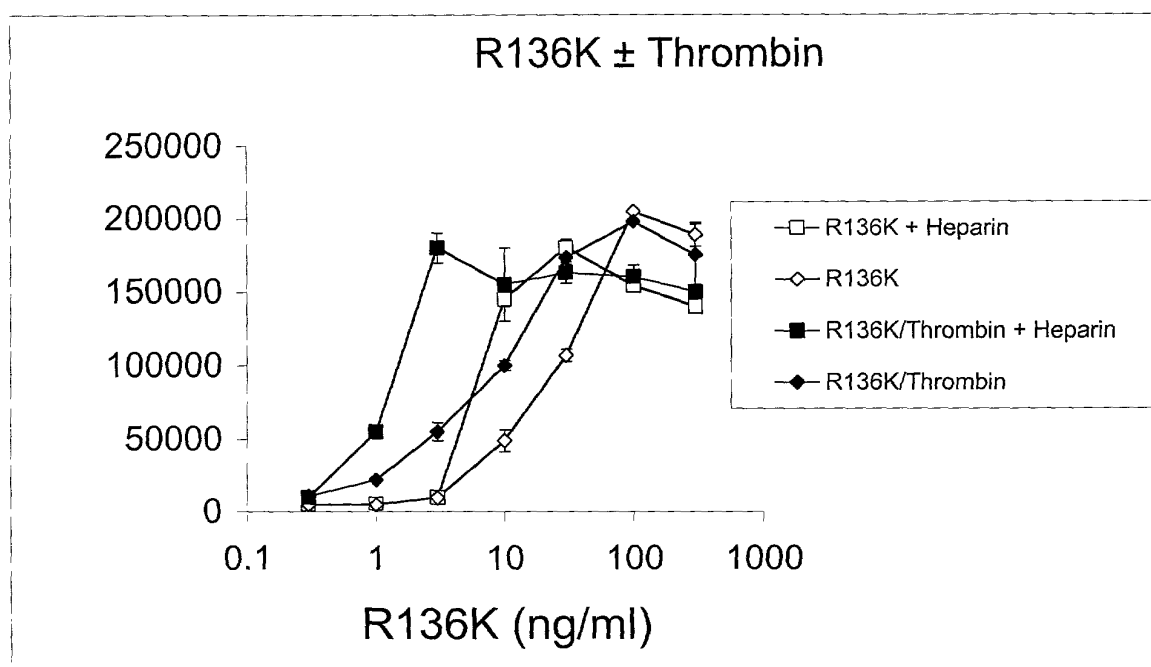


FIGURE 3

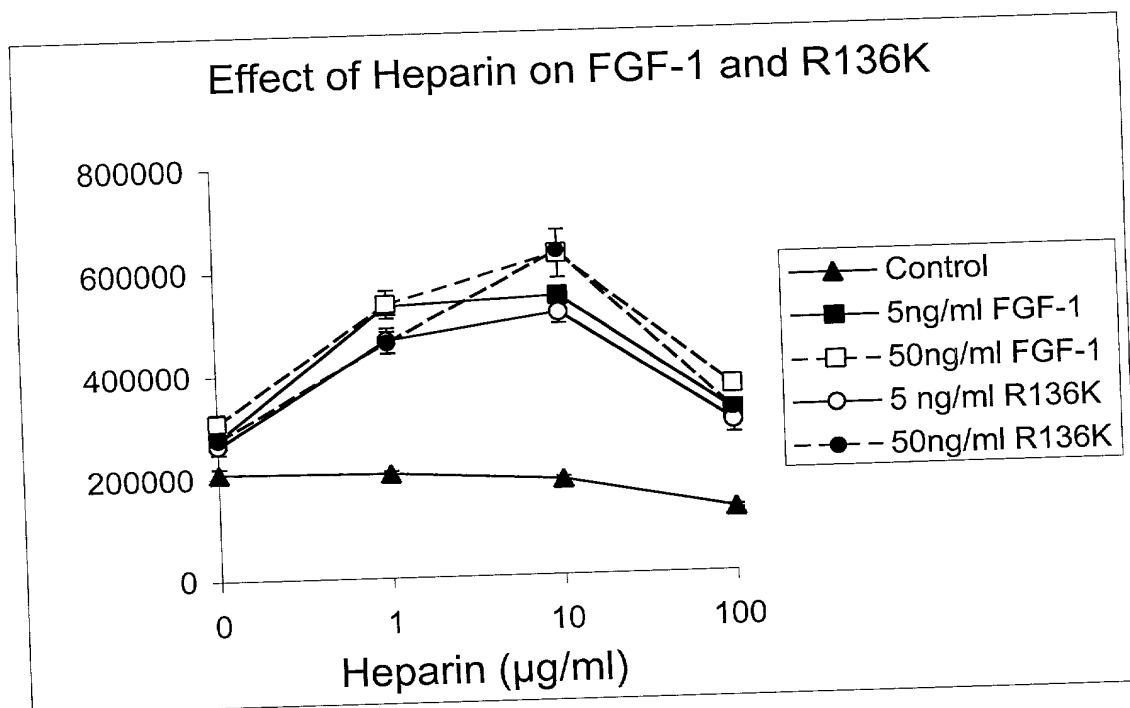


FIGURE 4

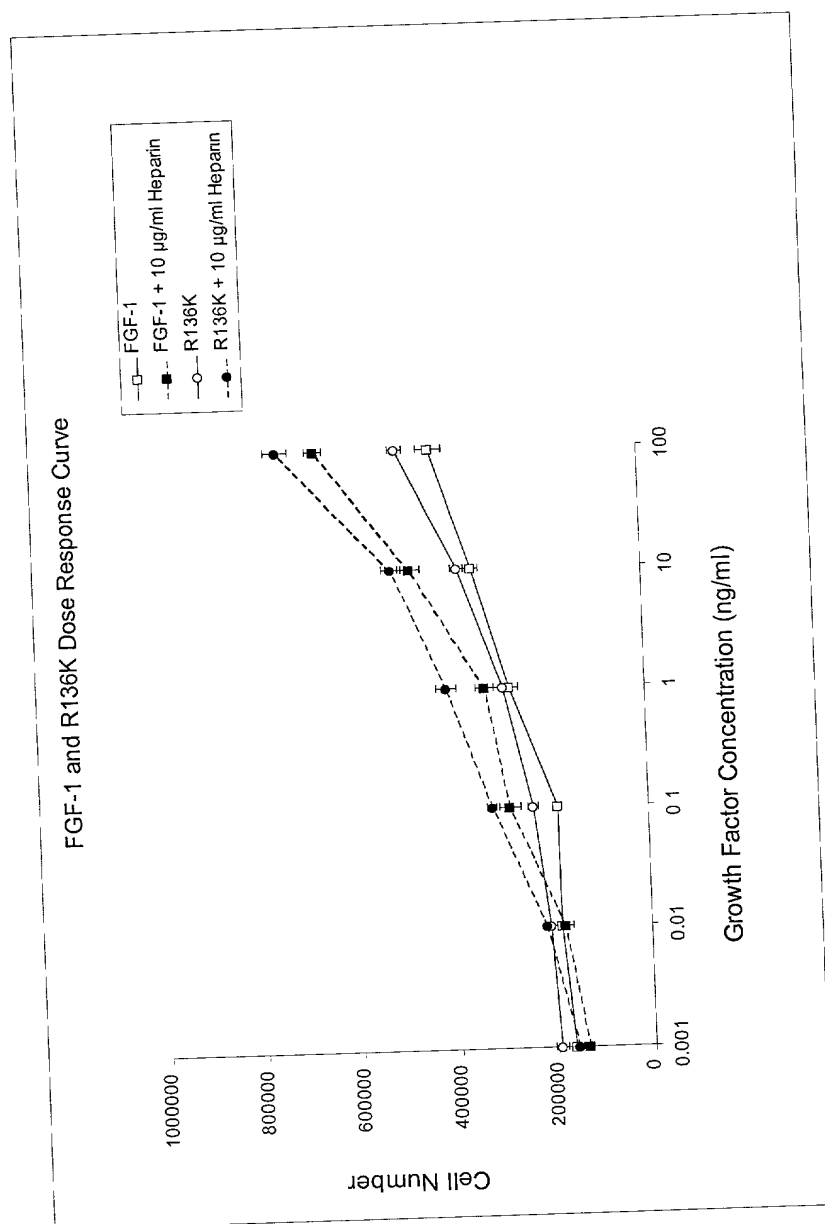


Figure 5

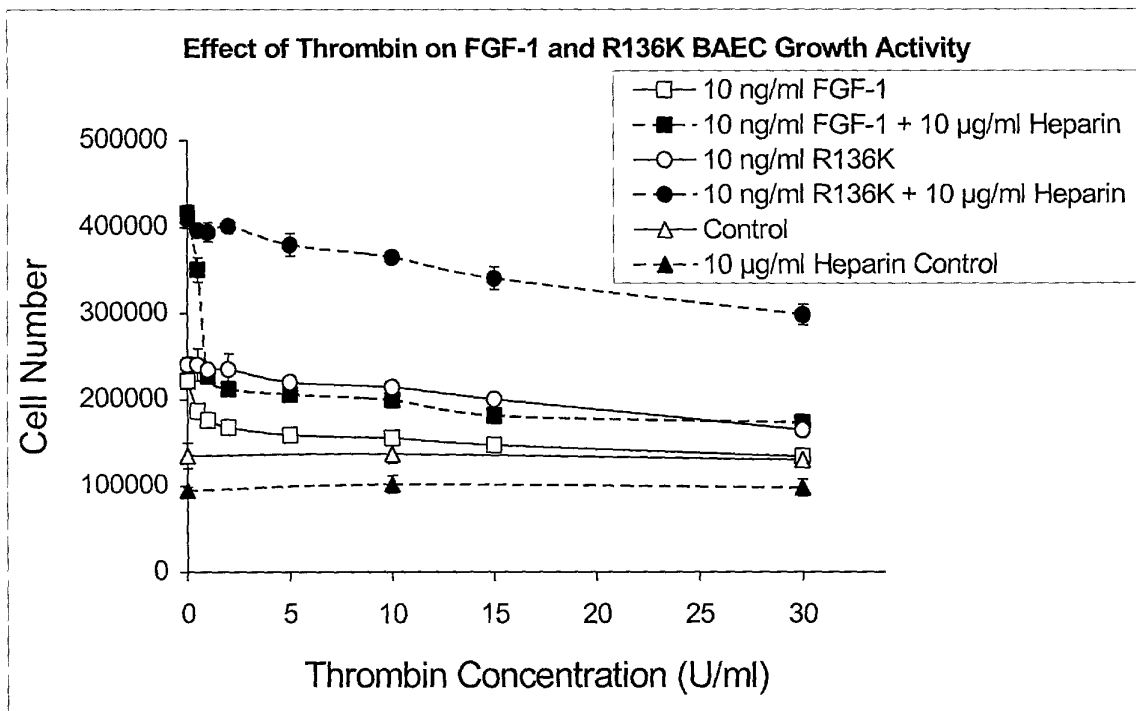


FIGURE 6

100354 4494

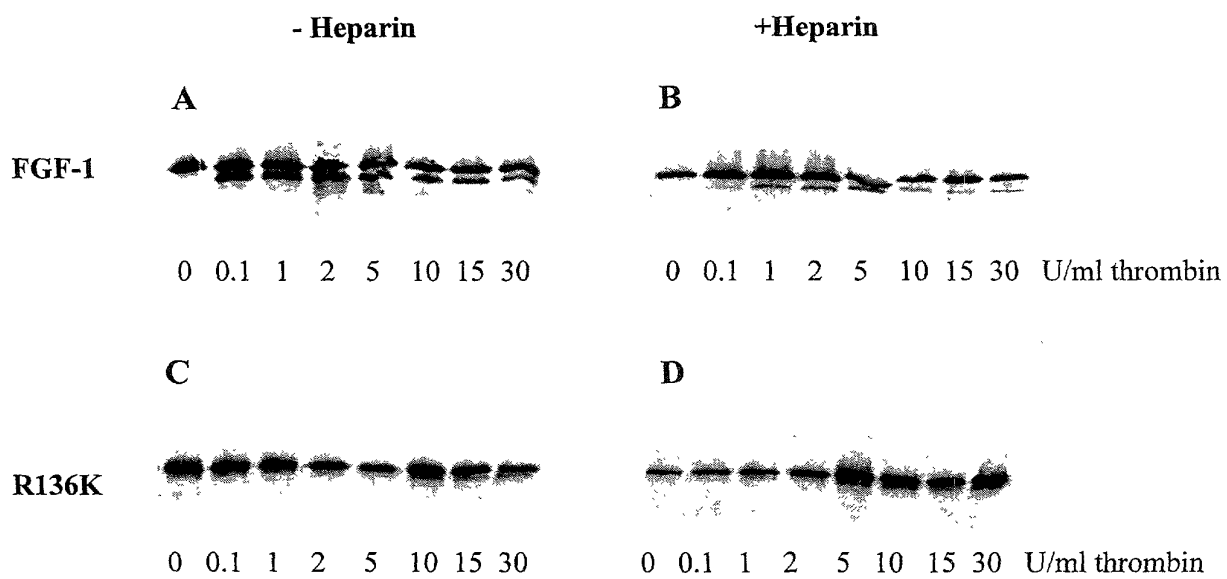


FIGURE 7

1002554-42204

GAATTCGGGA	ACGCGCCACA	AGCAGCAGCT	GCTGAGCCAT
GGCTGAAGGG	GAAATCACCA	CCTTCACAGC	CCTGACCGAG
AAGTTTAATC	TGCCTCCAGG	GAATTACAAG	AAGCCCAAAC
TCCTCTACTG	TAGCAACGGG	GGCCACTTCC	TGAGGATCCT
TCCGGATGGC	ACAGTGGATG	GGACAAGGGA	CAGGAGCGAC
CAGCACATTC	AGCTGCAGCT	CAGTGC GGAA	AGCGTG GGGG
AGGTGTATAT	AAAGAGTACC	GAGACTGGCC	AGTACTTGGC
CATGGACACC	GACGGGCTTT	TATACGGCTC	ACAGACACCA
AATGAGGAAT	GTTTGTTCCT	GGAAAGGCTG	GAGGAGAACC
ATTACAACAC	CTATATATCC	AAGAAGCATG	CAGAGAAGAA
TTGGTTTGTT	GGCCTCAAGA	AGAATGGGAG	CTGCAAACGC
GGTCCTAAAA	CTCACTATGG	CCAGAAAGCA	ATCTTGTTTC
TCCCCCTGCC	AGTCTCTTCT	GATTAAAGAG	ATCTGTTCTG
GTGTTGACCA	CTCCAGAGAA	GTTTCGAGGG	GTCCTCACCT
GGTTGACCCC	AAAAATGTTC	CCTTGACCAT	TGGCTGCGCT
AACCCCCAGC	CCACAGAGCC	TGAATTTGTA	AGCAACTT

FIGURE 10

AEGEITTFTA LTEKFNLPPG NYKKPKLLYC SNGGHFLRIL
PDGTVDGTRD RSDQHIQLQL SAESVGEVYI KSTETGQYLA
MDTDGLLYGS QTPNEECLFL ERLEENHYNT YISKKHAEKN
WVVG LKKN GS CKRGPKTHYG QKAILFLPLP VSSD

FIGURE 11

100254 4701
"452200"